COURSE NAME	**Algorithms in Bioinformatics**					
Code	PMIE20	Year of study	1st year of graduate study			
Course teacher	Ivo Ugrina	Credits (ECTS)	6			
Associate teachers		Type of instruction (number of hours)	L	S	E	
			30		30	
Status of the course	REQUIRED AND ELECTED COURSE	Percentage of application of e-learning	0%			

COURSE DESCRIPTION

Course objectives	Course objective is to introduce basic concepts and methods from computer science in applications to biomedicine and biology.
Course enrolment requirements and entry competences required for the course	Course enrolment requirement: Intermediate knowledge of data structures and algorithms. Intermediate knowledge of programming. Recommended previous knowledge: An introductory course in Statistics and Probability.
Learning outcomes expected at the level of the course (4 to 10 learning outcomes)	Students will: - know how dynamic programming (DP) can be used to solve string comparison problems such as "longest common subsequence", "edit distance", "local alignment", and "global alignment". - know how the DP solution for aligning two strings can be extended to aligning multiple strings. - know how k-mer indexes can be used for exact and approximate string search - know how sequence assembly is working - Know what hidden Markov-models (HMM) are, how these can be used to model and identify properties of strings, and how the Viterbi, forward, and backward HMM algorithms work. - will be able to implement known algorithms and data structures used in bioinformatics and apply them on real data. - recognize variants of known problems and adapt known algorithms to solve these variant problems. - choose between alternative solutions and use the solution that is most appropriate to solve a set of problems involving real data.
Course content broken down in detail by weekly class schedule (syllabus)	- Introduction to Basic Biology Concepts - Basic Statistics for Bioinformatics - Genome Sequencing - Dynamic Programming - Greedy Algorithms - String Distances - Motif Discovery - Sequence Alignment

	- Taxonomic Classification (Clustering) - Metagenomics and Genome Assembly
Format of instruction	Lectures and exercises section
Student responsibilities	Students are obliged to regularly attend lectures and exercises.
Screening student work *(name the proportion of ECTS credits for each activity so that the total number of ECTS credits is equal to the ECTS value of the course)*	Attending lectures and exercises (2) Written final exam/mid-term exams (2) Oral exam (2)
Grading and evaluating student work in class and at the final exam	One mid-term and one final exam. Passing these exams enables students to take an oral exam. Successfully passing the oral exam leads to successful completion of the course. Final grade is derived as the arithmetic mean of scores in mid-term/final exams (or a written exam) and the oral exam. In the case of failure in mid-term/final exams or the oral exam students must undergo a written exam before approaching oral exam again.
Required literature (available in the library and via other media)	1. P.Compeau, P. Pevzner, *“Bioinformatics Algorithms: An Active Learning Approach”*, 2018, Active Learning Publishers
Optional literature (at the time of submission of study programme proposal)	1. M. Rocha, P.G. Ferreira, *“Bioinformatics Algorithms: Design and Implementation in Python”*, 2018, Academic Press 2. http://rosalind.info
Quality assurance methods that ensure the acquisition of exit competences	Detailed statistics of student results, gathering feedback from students through official questionnaires and lecturer’s self-evaluation.
Other (as the proposer wishes to add)	